

# Preface

The 13th annual edition of the international meeting on Computational Intelligence methods for Bioinformatics and Biostatistics (CIBB 2016) built upon the tradition of the CIBB conference series and provided a multi-disciplinary forum open to researchers interested in the application of computational intelligence, in a broad sense, to open problems in bioinformatics, biostatistics, systems and synthetic biology, medical informatics, as well as computational approaches to life sciences in general.

In line with the spirit of CIBB, the 2016 meeting brought together researchers from different communities who address problems from different, but connected and often overlapping, perspectives. CIBB 2016 tackled the difficult task of bridging different backgrounds by providing an inclusive venue to discuss advances and future perspectives in different areas. It also fostered interaction between theory and practice, addressing both the theories underpinning the methodologies used to model and analyze biological systems, the practical applications of such theories, and the supporting technologies. Accordingly, participants at CIBB 2016 came from mathematical, computational, and medical backgrounds and institutions, both from academia and the private sector, offering collaboration opportunities and novel results in the areas of computational life sciences.

CIBB 2016 also offered a view on emerging and strongly developing trends and future opportunities at the edge of mathematics, computer and life sciences, such as synthetic biology, statistical investigation of genomic data, and applications to the understanding of complex diseases, such as cancer, and therapy opportunities. Along these lines, six keynote speakers, prominent scholars in their fields, presented the latest advances of their research within the context of their area of interest, and provided insights into open problems and future directions of general interest for the field. While papers in the main conference track addressed a rich set of open problems at the forefront of current research, the conference hosted six further special sessions on specific themes: biomedical databases, synthetic cell biology, high-performance computing in genetics, modelling for systems biology and medicine, survival analysis, and statistical inference in biological models. Researchers from Europe, Asia, USA, and Africa attended the conference. CIBB 2016 was made possible by the efforts of the Organizing, Program, and Steering Committees and by the support of sponsors and participants. CIBB 2016 was held in Stirling, UK, during September 1–3, 2016 (<http://www.cs.stir.ac.uk/events/cibb2016/>). With the continued support of the community, the next edition of CIBB will be held in Cagliari, Italy.

Overall, 61 contributions were submitted for consideration to CIBB 2016, amongst which 49 were invited for an oral presentation at the conference, after a first round of reviews (at this stage, each paper received an average of 3.7 reviews from the Program Committee and about 30 additional referees). Following the conference, selected papers were invited for further submission, after feedback and discussion from the conference.

This volume collects the papers that were accepted after a further round of reviews (2.5 for each paper, on average).

From 2004 to 2007, CIBB had the format of a special session of larger conferences, namely, WIRN 2004 in Perugia, WILF 2005 in Crema, FLINS 2006 in Genoa, and WILF 2007 in Camogli. Given the great success of the special session at WILF 2007 that included 26 strongly rated papers, the Steering Committee decided to turn CIBB into an autonomous conference starting with the 2008 edition in Vietri. The following editions in Italian venues were held in Genoa (2009), Palermo (2010), and Gargnano (2011). Until 2012, CIBB meetings were held annually in Italy with an increasing number of participants. CIBB 2012 was the first edition organized outside Italy, in Houston, then in Nice, France (2013), Cambridge, UK (2014), and Naples, Italy (2015). A rigorous peer-review selection process is applied every time to ultimately select the papers included in the program of the conference, in the conference proceedings published in the LNBI-LNCS book series by Springer, and in some cases, selected papers were published in special issues of well-qualified international journals, such as *BMC Bioinformatics*.

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